

BCS 03-5005_PCT-SEQUENZPROTOKOLL.ST25
SEQUENCE LISTING

<110> Bayer CropScience GmbH

<120> Plants with increased activity of a Class 3 branching enzyme

<130> BCS 03-5005-PCT

<150> EP 03090324.9

<151> 2003-09-30

<160> 6

<170> PatentIn version 3.1

<210> 1

<211> 1004

<212> DNA

<213> Solanum tuberosum

<400> 1
tcaaactagt cacaaccagt ccatttctgg aggtcgttcc ttcgcagaaa tactgattgg 60
taactccttg gggaaatcct ccatatcaca agagtcatta cttagaggct gtcggttaca 120
caagatgatac agattaatta catctacaat tgggtggcat gcataacctca acttcatggg 180
caatgaattt ggtcacccaa agagagtaga gtttccaatg tcaagcaaca atttctcctt 240
ttcactggct aaccgtcgct gggatctatt ggaagatgtt gtacattatc aattgttctc 300
atttgataag ggtatgatgg acttggataa aaatgggaga attttgtcca gaggtcttgc 360
caacattcac catgtcaatg atactaccat ggtgatttct tacttgagag gtcccaatct 420
ctttgtgttc aactttcatc ctgtcaattc atatgaaaga tacattatag gtgtggaaga 480
agctggagag tatcaagtca cattaaatac agatgaaaac aagtatggtg gtagaggact 540
acttggccat gatcagaata ttcaaagaac cattagtaga agagctgatg gaatgagatt 600
ttgcttggaa gtgcctctgc caagtagaag tgctcaggct tacaagttga cccgaattct 660
aagagcatga tcactctagt aatcaaagt cctcatatga tgacacaaaa ggaaagggtc 720
tacattgccc ttacttgat caatattgac acctttccga ggtgagtttc tgtgattctt 780
gagcagactg ttggctagtc aattatcatg aacttttgcc ttcagcatcc ggatagtcgc 840

BCS 03-5005_PCT-SEQUENZPROTOKOLL.ST25

ttctcctgtg caatgagggc atggacgaat ttttttttgg cttgtcatgg gggtcataag 900
 catccgccag attaagattt cacaggcctc gagtaaaacc atcacttact ttaaggatac 960
 acaaacacac caacgggggtg caggctctga taccttctaa agtg 1004

<210> 2

<211> 2096

<212> DNA

<213> Solanum tuberosum

<400> 2

aacaatgctc tctctgtcgg attcaattcg aatttcttca ccattgagcg attctcgtct 60
 tagttttcta tctcaaaccg gaagcagaac cagtcgccag cttaaatttg ttcgcagccg 120
 ccgggctcga gtttcgaggt gtagatgctc agcaacggag caaccgccac cgcaacgacg 180
 gaagcaacga ccggagaagt acaaacagtc ggaggaaggg aaaggaatcg atcctgttgg 240
 atttctcagc aaatacggca ttactcataa agcgtttgct caatttcttc gtgaaagata 300
 taaatcattg aaggacttga aggatgaaat attgactcgt catttcagtc tcaaggagat 360
 gtctaactggg tatgaattaa tgggtatgca tcgcaacata caacatcgag tggatttctt 420
 ggaatgggct ccagggtgctc gctactgtgc tctgattggg gacttcaatg ggtggtcaac 480
 aactggtaac tgtgccagag agggtcattt tggtcatgac gattatgggt attggtttat 540
 tattcttgaa gataaattac gtgaaggaga agaacctgat aaattgtatt ttcaacagta 600
 caattatgcg gaggactatg gtaaagggtga cacgggtatt accgtcgagg aaatctttaa 660
 aaaagcaaat gatgagtatt gggaacctgg agaagatcgc ttcattaaat cacgttatga 720
 ggtggcagca aagttatatg aggaaatggt cggaccaaat ggacctcaaa cagaagagga 780
 actagaagca atgcctgatg cagctacacg atacaaaact tggaaagagc aacaaaaaga 840
 ggatccggca agcaatttgc catcgtatga tgtggtagat agtggaagaa aatatgatat 900
 ttacaatatt ataggtgatc ctgaatcgtt taagaaattt cgtatgaaac agcctcctat 960
 tgcttactgg ttagaaacta aaaagggag gaaaggctgg ttacagaaat atatgcctgc 1020
 tttacctcat ggaagcaaat acagggtgta ttttaacaca ccaaatgggc ctcttgaacg 1080
 agttcctgcg tgggcccaatt ttgtcattcc agatgcaggc gggatggcat tagcagtcca 1140
 ttgggaacca cctcctgaat atgcttataa atggaaacac aagctaccag tcaagcctaa 1200
 gtctttgcgc atatatgaat gtcatgttgg catctctggc caggaaccaa aagtttcatc 1260
 tttcaatgat tttattagca aggtccttcc gcatgtaaaa gaagctggat acaatgcaat 1320
 acaaatattt ggagttgttg agcacaagga ttatttctact gttggatata gagtgaccaa 1380
 tttttatgct gttagtagcc gttatggcac accggatgac ttcaagcgct tggttgatga 1440
 agcatatggg cttggactgc ttgtcttttt ggagattgtg cactcttatg cagcagcaga 1500

<400> 3																60
gaattgtaat acgactcact atagggcgaa ttgggccctc tagatgcatg ctcgagcggc																116
cgccagtgtg atggatatct gcagaattcg gcttaaca atg ctc tct ctg tcg gat																
Met Leu Ser Leu Ser Asp																
1 5																
tca att cga att tct tca cca ttg agc gat tct cgt ctt agt ttt cta																164
Ser Ile Arg Ile Ser Ser Pro Leu Ser Asp Ser Arg Leu Ser Phe Leu																
10 15 20																
tct caa acc gga agc aga acc agt cgc cag ctt aaa ttt gtt cgc agc																212
Ser Gln Thr Gly Ser Arg Thr Ser Arg Gln Leu Lys Phe Val Arg Ser																
25 30 35																
cgc cgg gct cga gtt tcg agg tgt aga tgc tca gca acg gag caa ccg																260
Arg Arg Ala Arg Val Ser Arg Cys Arg Cys Ser Ala Thr Glu Gln Pro																
40 45 50																
cca ccg caa cga cgg aag caa cga ccg gag aag tac aaa cag tcg gag																308
Pro Pro Gln Arg Arg Lys Gln Arg Pro Glu Lys Tyr Lys Gln Ser Glu																
55 60 65 70																
gaa gag aaa gga atc gat cct gtt gga ttt ctc agc aaa tac ggc att																356
Glu Glu Lys Gly Ile Asp Pro Val Gly Phe Leu Ser Lys Tyr Gly Ile																
75 80 85																

BCS 03-5005_PCT-SEQUENZPROTOKOLL.ST25

act cat aaa gcg ttt gct caa ttt ctt cgt gaa aga tat aaa tca ttg	404
Thr His Lys Ala Phe Ala Gln Phe Leu Arg Glu Arg Tyr Lys Ser Leu	
90 95 100	
aag gac ttg aag gat gaa ata ttg act cgt cat ttc agt ctc aag gag	452
Lys Asp Leu Lys Asp Glu Ile Leu Thr Arg His Phe Ser Leu Lys Glu	
105 110 115	
atg tct act ggg tat gaa tta atg ggt atg cat cgc aac ata caa cat	500
Met Ser Thr Gly Tyr Glu Leu Met Gly Met His Arg Asn Ile Gln His	
120 125 130	
cga gtg gat ttc ttg gaa tgg gct cca ggt gct cgc tac tgt gct ctg	548
Arg Val Asp Phe Leu Glu Trp Ala Pro Gly Ala Arg Tyr Cys Ala Leu	
135 140 145 150	
att ggt gac ttc aat ggg tgg tca aca act ggt aac tgt gcc aga gag	596
Ile Gly Asp Phe Asn Gly Trp Ser Thr Thr Gly Asn Cys Ala Arg Glu	
155 160 165	
ggg cat ttt ggt cat gac gat tat ggg tat tgg ttt att att ctt gaa	644
Gly His Phe Gly His Asp Asp Tyr Gly Tyr Trp Phe Ile Ile Leu Glu	
170 175 180	
gat aaa tta cgt gaa gga gaa gaa cct gat aaa ttg tat ttt caa cag	692
Asp Lys Leu Arg Glu Gly Glu Glu Glu Pro Asp Lys Leu Tyr Phe Gln Gln	
185 190 195	
tac aat tat gcg gag gac tat gat aaa ggt gac acg ggt att acc gtc	740
Tyr Asn Tyr Ala Glu Asp Tyr Asp Lys Gly Asp Thr Gly Ile Thr Val	
200 205 210	
gag gaa atc ttt aaa aaa gca aat gat gag tat tgg gaa cct gga gaa	788
Glu Glu Ile Phe Lys Lys Ala Asn Asp Glu Tyr Trp Glu Pro Gly Glu	
215 220 225 230	
gat cgc ttc att aaa tca cgt tat gag gtg gca gca aag tta tat gag	836
Asp Arg Phe Ile Lys Ser Arg Tyr Glu Val Ala Ala Lys Leu Tyr Glu	
235 240 245	
gaa atg ttc gga cca aat gga cct caa aca gaa gag gaa cta gaa gca	884
Glu Met Phe Gly Pro Asn Gly Pro Gln Thr Glu Glu Glu Leu Glu Ala	
250 255 260	
atg cct gat gca gct aca cga tac aaa act tgg aaa gag caa caa aaa	932
Met Pro Asp Ala Ala Thr Arg Tyr Lys Thr Trp Lys Glu Gln Gln Lys	
265 270 275	
aag gat ccg gca agc aat ttg cca tcg tat gat gtg gta gat agt gga	980
Lys Asp Pro Ala Ser Asn Leu Pro Ser Tyr Asp Val Val Asp Ser Gly	
280 285 290	
aaa gaa tat gat att tac aat att ata ggt gat cct gaa tcg ttt aag	1028
Lys Glu Tyr Asp Ile Tyr Asn Ile Ile Gly Asp Pro Glu Ser Phe Lys	
295 300 305 310	
aaa ttt cgt atg aaa cag cct cct att gct tac tgg tta gaa act aaa	1076
Lys Phe Arg Met Lys Gln Pro Pro Ile Ala Tyr Trp Leu Glu Thr Lys	
315 320 325	
aag gga agg aaa ggc tgg tta cag aaa tat atg cct gct tta cct cat	1124
Lys Gly Arg Lys Gly Trp Leu Gln Lys Tyr Met Pro Ala Leu Pro His	
330 335 340	
gga agc aaa cac agg gtg tat ttt aac aca cca aat ggg cct ctt gaa	1172
Gly Ser Lys His Arg Val Tyr Phe Asn Thr Pro Asn Gly Pro Leu Glu	
345 350 355	

BCS 03-5005_PCT-SEQUENZPROTOKOLL.ST25

cga Arg 360	gtt Val	cct Pro	gcg Ala	tgg Trp	gcc Ala 365	aat Asn 365	ttt Phe	gtc Val	att Ile	cca Pro 370	gat Asp 370	gca Ala	gac Asp	ggg Gly	atg Met	1220
gca Ala 375	tta Leu	gca Ala	gtc Val	cat His 380	tgg Trp 380	gaa Glu	cca Pro	cct Pro	cct Pro	gaa Glu 385	tat Tyr	gct Ala	tat Tyr	aaa Lys	tgg Trp 390	1268
aaa Lys	cac His	aag Lys	cta Leu	cca Pro 395	gtc Val	aag Lys	cct Pro	aag Lys	tcc Ser 400	ttg Leu	cgc Arg	ata Ile	tat Tyr	gaa Glu 405	tgt Cys	1316
cat His	gtt Val	ggc Gly	atc Ile 410	tct Ser	ggc Gly	cag Gln	gaa Glu	cca Pro 415	aaa Lys	gtt Val	tca Ser	tct Ser	ttc Phe 420	aat Asn	gat Asp	1364
ttt Phe	att Ile	agc Ser 425	aag Lys	gtc Val	ctt Leu	ccg Pro	cat His 430	gta Val	aaa Lys	gaa Glu	gct Ala	gga Gly 435	tac Tyr	aat Asn	gca Ala	1412
acg Thr	caa Gln 440	att Ile	att Ile	gga Gly	gtt Val	gtt Val 445	gag Glu	cac His	aag Lys	gat Asp	tat Tyr 450	ttc Phe	act Thr	gtt Val	gga Gly	1460
tat Tyr 455	aga Arg	gtg Val	acc Thr	aat Asn	ttt Phe 460	tat Tyr	gct Ala	gtt Val	agt Ser	agc Ser 465	cgf Arg	tat Tyr	ggc Gly	aca Thr	ccg Pro 470	1508
gat Asp	gac Asp	ttc Phe	aag Lys	cgf Arg 475	ttg Leu	gtt Val	gat Asp	gaa Glu	gca Ala 480	cat His	ggg Gly	ctt Leu	gga Gly	ctg Leu 485	ctt Leu	1556
gtc Val	ttt Phe	ttg Leu	gag Glu 490	att Ile	gtg Val	cac His	tcc Ser	tat Tyr 495	gca Ala	gca Ala	gca Ala	gat Asp	gaa Glu 500	atg Met	gtt Val	1604
ggg Gly	tta Leu	tct Ser 505	ctt Leu	ttt Phe	gat Asp	gga Gly	gca Ala 510	aat Asn	gat Asp	tgc Cys	tat Tyr	ttc Phe 515	cac His	act Thr	ggt Gly	1652
aaa Lys	cgf Arg 520	gga Gly	cac His	cac His	aaa Lys	ttc Phe 525	tgg Trp	ggc Gly	aca Thr	cgf Arg	atg Met 530	ttc Phe	aaa Lys	tat Tyr	gga Gly	1700
gat Asp 535	cct Pro	gat Asp	gtt Val	ctg Leu	cac His 540	ttt Phe	ctt Leu	ctt Leu	tca Ser	aat Asn 545	ctg Leu	aac Asn	tgg Trp	tgg Trp	gtg Val 550	1748
gag Glu	gag Glu	tat Tyr	cat His	gtc Val 555	gat Asp	ggc Gly	ttc Phe	cat His	ttt Phe 560	cat His	tcg Ser	ctc Leu	tcg Ser	tcc Ser 565	atg Met	1796
ttg Leu	tat Tyr	acg Thr	cat His 570	aat Asn	gga Gly	ttt Phe	gct Ala	tca Ser 575	ttt Phe	act Thr	ggt Gly	gac Asp	atg Met 580	gat Asp	gaa Glu	1844
tac Tyr	tgt Cys	aac Asn 585	caa Gln	tat Tyr	gtt Val	gac Asp	aag Lys 590	gag Glu	gcc Ala	tta Leu	ttg Leu	tac Tyr 595	ctc Leu	ata Ile	tta Leu	1892
gca Ala 600	aat Asn	gaa Glu	gta Val	tta Leu	cat His	gct Ala 605	ctt Leu	cat His	cct Pro	aat Asn	gtg Val 610	atc Ile	acg Thr	att Ile	gct Ala	1940
gtg Val 615	gat Asp	gca Ala	act Thr	ctg Leu	tat Tyr 620	cct Pro	gga Gly	ctc Leu	tgc Cys	gat Asp 625	cca Pro	aca Thr	tct Ser	caa Gln	ggt Gly 630	1988

BCS 03-5005_PCT-SEQUENZPROTOKOLL.ST25

gga ctg ggc ttt gat tat ttt gcc aat ctt tct gcc tca gag atg tgg Gly Leu Gly Phe Asp Tyr Phe Ala Asn Leu Ser Ala Ser Glu Met Trp 635 640 645	2036
ctt gca tta ctt gaa aat act cct gat cat gaa tgg tgc atg agt aag Leu Ala Leu Leu Glu Asn Thr Pro Asp His Glu Trp Cys Met Ser Lys 650 655 660	2084
att gtt agc aca tta gtg ggc gat aga caa aat act gat aaa atg ctt Ile Val Ser Thr Leu Val Gly Asp Arg Gln Asn Thr Asp Lys Met Leu 665 670 675	2132
ttg tat gca gaa aat cac aac cag tcc att tct gga ggt cgt tcc ttc Leu Tyr Ala Glu Asn His Asn Gln Ser Ile Ser Gly Gly Arg Ser Phe 680 685 690	2180
gca gaa ata ctg att ggt aac tcc ttg ggg aaa tct tcc ata tca caa Ala Glu Ile Leu Ile Gly Asn Ser Leu Gly Lys Ser Ser Ile Ser Gln 695 700 705 710	2228
gag tca tta ctt aga ggc tgc tcg tta cac aag atg atc aga tta att Glu Ser Leu Leu Arg Gly Cys Ser Leu His Lys Met Ile Arg Leu Ile 715 720 725	2276
aca tct aca att ggt ggt cat gca tac ctc aac ttc atg ggc aat gaa Thr Ser Thr Ile Gly Gly His Ala Tyr Leu Asn Phe Met Gly Asn Glu 730 735 740	2324
ttt ggt cac cca aag aga gta gag ttt cca atg tca agc aac aat ttc Phe Gly His Pro Lys Arg Val Glu Phe Pro Met Ser Ser Asn Asn Phe 745 750 755	2372
tcc ttt tca ctg gct aac cgt cgc tgg gat cta ttg gaa gat gtt gta Ser Phe Ser Leu Ala Asn Arg Arg Trp Asp Leu Leu Glu Asp Val Val 760 765 770	2420
cat tat caa tta ttc tca ttt gat aag gat atg atg gac ttg gat aaa His Tyr Gln Leu Phe Ser Phe Asp Lys Asp Met Met Asp Leu Asp Lys 775 780 785 790	2468
aat ggg aga att ttg tcc aga ggt ctt gcc aac att cac cat gtc aat Asn Gly Arg Ile Leu Ser Arg Gly Leu Ala Asn Ile His His Val Asn 795 800 805	2516
gat act acc atg gtg att tct tac ttg aga ggt ccc aat ctc ttt gtg Asp Thr Thr Met Val Ile Ser Tyr Leu Arg Gly Pro Asn Leu Phe Val 810 815 820	2564
ttc aac ttt cat cct gtc aat tca tat gaa aga tac att ata ggt gtg Phe Asn Phe His Pro Val Asn Ser Tyr Glu Arg Tyr Ile Ile Gly Val 825 830 835	2612
gaa gaa gct gga gag tat caa gtc aca tta aat aca gat gaa aac aag Glu Glu Ala Gly Glu Tyr Gln Val Thr Leu Asn Thr Asp Glu Asn Lys 840 845 850	2660
tat ggt ggt aga gga cta ctt ggc cat gat cag aat act caa aga acc Tyr Gly Gly Arg Gly Leu Leu Gly His Asp Gln Asn Thr Gln Arg Thr 855 860 865 870	2708
att agt aga aga gct gat gga atg aga ttt tgc ttg gaa gta cct ctg Ile Ser Arg Arg Ala Asp Gly Met Arg Phe Cys Leu Glu Val Pro Leu 875 880 885	2756
cca agt aga agt gct cag gtc tac aag ttg acc cga att cta aga gca Pro Ser Arg Ser Ala Gln Val Tyr Lys Leu Thr Arg Ile Leu Arg Ala 890 895 900	2804

BCS 03-5005_PCT-SEQUENZPROTOKOLL.ST25

tgatcactct agcaatcaaa gtgcctcata tgatcacaca aaaggggaagg ttctacattg 2864
 Cccttatact gaccaatatt gtggcctttc cgagggtgagt ttctgtgatt cttgagcaca 2924
 ggctgttggc tagtcagtta tcatgaactt ttgccttcag catctggata agcgcttctc 2984
 ctgtgcaatg agggcatgga cgaaattttt ttggttcgtc atgggagtca aaagcatctg 3044
 ccagattaag atttcacagg cctcgagtaa aaccatcact tacttaggat acacaaacac 3104
 atcaacgggg tgcaggctct gataccttct aaagtgaagc cgaattccag cacactggcg 3164
 gccgttacta gtggatccga gctcggtacc aagcttggcg 3204

<210> 4

<211> 902

<212> PRT

<213> solanum tuberosum

<400> 4

Met Leu Ser Leu Ser Asp Ser Ile Arg Ile Ser Ser Pro Leu Ser Asp
 1 5 10 15

Ser Arg Leu Ser Phe Leu Ser Gln Thr Gly Ser Arg Thr Ser Arg Gln
 20 25 30

Leu Lys Phe Val Arg Ser Arg Arg Ala Arg Val Ser Arg Cys Arg Cys
 35 40 45

Ser Ala Thr Glu Gln Pro Pro Pro Gln Arg Arg Lys Gln Arg Pro Glu
 50 55 60

Lys Tyr Lys Gln Ser Glu Glu Glu Lys Gly Ile Asp Pro Val Gly Phe
 65 70 75 80

Leu Ser Lys Tyr Gly Ile Thr His Lys Ala Phe Ala Gln Phe Leu Arg
 85 90 95

Glu Arg Tyr Lys Ser Leu Lys Asp Leu Lys Asp Glu Ile Leu Thr Arg
 100 105 110

His Phe Ser Leu Lys Glu Met Ser Thr Gly Tyr Glu Leu Met Gly Met
 115 120 125

His Arg Asn Ile Gln His Arg Val Asp Phe Leu Glu Trp Ala Pro Gly
 130 135 140

Ala Arg Tyr Cys Ala Leu Ile Gly Asp Phe Asn Gly Trp Ser Thr Thr
 145 150 155 160

BCS 03-5005_PCT-SEQUENZPROTOKOLL.ST25

Glu Ala Gly Tyr Asn Ala Thr Gln Ile Ile Gly Val Val Glu His Lys
 435 440 445

Asp Tyr Phe Thr Val Gly Tyr Arg Val Thr Asn Phe Tyr Ala Val Ser
 450 455 460

Ser Arg Tyr Gly Thr Pro Asp Asp Phe Lys Arg Leu Val Asp Glu Ala
 465 470 475 480

His Gly Leu Gly Leu Leu Val Phe Leu Glu Ile Val His Ser Tyr Ala
 485 490 495

Ala Ala Asp Glu Met Val Gly Leu Ser Leu Phe Asp Gly Ala Asn Asp
 500 505 510

Cys Tyr Phe His Thr Gly Lys Arg Gly His His Lys Phe Trp Gly Thr
 515 520 525

Arg Met Phe Lys Tyr Gly Asp Pro Asp Val Leu His Phe Leu Leu Ser
 530 535 540

Asn Leu Asn Trp Trp Val Glu Glu Tyr His Val Asp Gly Phe His Phe
 545 550 555 560

His Ser Leu Ser Ser Met Leu Tyr Thr His Asn Gly Phe Ala Ser Phe
 565 570 575

Thr Gly Asp Met Asp Glu Tyr Cys Asn Gln Tyr Val Asp Lys Glu Ala
 580 585 590

Leu Leu Tyr Leu Ile Leu Ala Asn Glu Val Leu His Ala Leu His Pro
 595 600 605

Asn Val Ile Thr Ile Ala Val Asp Ala Thr Leu Tyr Pro Gly Leu Cys
 610 615 620

Asp Pro Thr Ser Gln Gly Gly Leu Gly Phe Asp Tyr Phe Ala Asn Leu
 625 630 635 640

Ser Ala Ser Glu Met Trp Leu Ala Leu Leu Glu Asn Thr Pro Asp His
 645 650 655

Glu Trp Cys Met Ser Lys Ile Val Ser Thr Leu Val Gly Asp Arg Gln
 660 665 670

Asn Thr Asp Lys Met Leu Leu Tyr Ala Glu Asn His Asn Gln Ser Ile
 675 680 685

Ser Gly Gly Arg Ser Phe Ala Glu Ile Leu Ile Gly Asn Ser Leu Gly
 690 695 700

10/18

BCS 03-5005_PCT-SEQUENZENPROTOKOLL.ST25

Lys Ser Ser Ile Ser Gln Glu Ser Leu Leu Arg Gly Cys Ser Leu His
 705 710 715 720

Lys Met Ile Arg Leu Ile Thr Ser Thr Ile Gly Gly His Ala Tyr Leu
 725 730 735

Asn Phe Met Gly Asn Glu Phe Gly His Pro Lys Arg Val Glu Phe Pro
 740 745 750

Met Ser Ser Asn Asn Phe Ser Phe Ser Leu Ala Asn Arg Arg Trp Asp
 755 760 765

Leu Leu Glu Asp Val Val His Tyr Gln Leu Phe Ser Phe Asp Lys Asp
 770 775 780

Met Met Asp Leu Asp Lys Asn Gly Arg Ile Leu Ser Arg Gly Leu Ala
 785 790 795 800

Asn Ile His His Val Asn Asp Thr Thr Met Val Ile Ser Tyr Leu Arg
 805 810 815

Gly Pro Asn Leu Phe Val Phe Asn Phe His Pro Val Asn Ser Tyr Glu
 820 825 830

Arg Tyr Ile Ile Gly Val Glu Glu Ala Gly Glu Tyr Gln Val Thr Leu
 835 840 845

Asn Thr Asp Glu Asn Lys Tyr Gly Gly Arg Gly Leu Leu Gly His Asp
 850 855 860

Gln Asn Thr Gln Arg Thr Ile Ser Arg Arg Ala Asp Gly Met Arg Phe
 865 870 875 880

Cys Leu Glu Val Pro Leu Pro Ser Arg Ser Ala Gln Val Tyr Lys Leu
 885 890 895

Thr Arg Ile Leu Arg Ala
 900

<210> 5

<211> 3047

<212> DNA

<213> solanum tuberosum

<220>

<221> CDS

<222> (5)..(2710)

BCS 03-5005_PCT-SEQUENZPROTOKOLL.ST25

<223>

<400> 5

aaca	atg	ctc	tct	ctg	tcg	gat	tca	att	cga	att	tct	tca	cca	ttg	agc	49
Met	Leu	Ser	Leu	Ser	Asp	Ser	Ile	Arg	Ile	Ser	Ser	Pro	Leu	Ser		
1				5					10					15		
gat	tct	cgt	ctt	agt	ttt	cta	tct	caa	acc	gga	agc	aga	acc	agt	cgc	97
Asp	Ser	Arg	Leu	Ser	Phe	Leu	Ser	Gln	Thr	Gly	Ser	Arg	Thr	Ser	Arg	
			20					25						30		
cag	ctt	aaa	ttt	gtt	cgc	agc	cgc	cgg	gct	cga	gtt	tcg	agg	tgt	aga	145
Gln	Leu	Lys	Phe	Val	Arg	Ser	Arg	Arg	Ala	Arg	Val	Ser	Arg	Cys	Arg	
			35					40					45			
tgc	tca	gca	acg	gag	caa	ccg	cca	ccg	caa	cga	cgg	aag	caa	cga	ccg	193
Cys	Ser	Ala	Thr	Glu	Gln	Pro	Pro	Pro	Gln	Arg	Arg	Lys	Gln	Arg	Pro	
		50				55						60				
gag	aag	tac	aaa	cag	tcg	gag	gaa	ggg	aaa	gga	atc	gat	cct	gtt	gga	241
Glu	Lys	Tyr	Lys	Gln	Ser	Glu	Glu	Gly	Lys	Gly	Ile	Asp	Pro	Val	Gly	
	65				70						75					
ttt	ctc	agc	aaa	tac	ggc	att	act	cat	aaa	gcg	ttt	gct	caa	ttt	ctt	289
Phe	Leu	Ser	Lys	Tyr	Gly	Ile	Thr	His	Lys	Ala	Phe	Ala	Gln	Phe	Leu	
80					85					90					95	
cgt	gaa	aga	tat	aaa	tca	ttg	aag	gac	ttg	aag	gat	gaa	ata	ttg	act	337
Arg	Glu	Arg	Tyr	Lys	Ser	Leu	Lys	Asp	Leu	Lys	Asp	Glu	Ile	Leu	Thr	
				100					105					110		
cgt	cat	ttc	agt	ctc	aag	gag	atg	tct	act	ggg	tat	gaa	tta	atg	ggt	385
Arg	His	Phe	Ser	Leu	Lys	Glu	Met	Ser	Thr	Gly	Tyr	Glu	Leu	Met	Gly	
			115					120					125			
atg	cat	cgc	aac	ata	caa	cat	cga	gtg	gat	ttc	ttg	gaa	tggt	gct	cca	433
Met	His	Arg	Asn	Ile	Gln	His	Arg	Val	Asp	Phe	Leu	Glu	Trp	Ala	Pro	
		130					135					140				
ggt	gct	cgc	tac	tgt	gct	ctg	att	ggt	gac	ttc	aat	ggg	tggt	tca	aca	481
Gly	Ala	Arg	Tyr	Cys	Ala	Leu	Ile	Gly	Asp	Phe	Asn	Gly	Trp	Ser	Thr	
	145					150					155					
act	ggt	aac	tgt	gcc	aga	gag	ggt	cat	ttt	ggt	cat	gac	gat	tat	ggg	529
Thr	Gly	Asn	Cys	Ala	Arg	Glu	Gly	His	Phe	Gly	His	Asp	Asp	Tyr	Gly	
160				165						170					175	
tat	tggt	ttt	att	att	ctt	gaa	gat	aaa	tta	cgt	gaa	gga	gaa	gaa	cct	577
Tyr	Trp	Phe	Ile	Ile	Leu	Glu	Asp	Lys	Leu	Arg	Glu	Gly	Glu	Glu	Pro	
				180					185						190	
gat	aaa	ttg	tat	ttt	caa	cag	tac	aat	tat	gcg	gag	gac	tat	ggt	aaa	625
Asp	Lys	Leu	Tyr	Phe	Gln	Gln	Tyr	Asn	Tyr	Ala	Glu	Asp	Tyr	Gly	Lys	
			195					200					205			
ggt	gac	acg	ggt	att	acc	gtc	gag	gaa	atc	ttt	aaa	aaa	gca	aat	gat	673
Gly	Asp	Thr	Gly	Ile	Thr	Val	Glu	Glu	Ile	Phe	Lys	Lys	Ala	Asn	Asp	
		210					215					220				
gag	tat	tggt	gaa	cct	gga	gaa	gat	cgc	ttc	att	aaa	tca	cgt	tat	gag	721
Glu	Tyr	Trp	Glu	Pro	Gly	Glu	Asp	Arg	Phe	Ile	Lys	Ser	Arg	Tyr	Glu	
	225					230					235					
gtg	gca	gca	aag	tta	tat	gag	gaa	atg	ttc	gga	cca	aat	gga	cct	caa	769
Val	Ala	Ala	Lys	Leu	Tyr	Glu	Glu	Met	Phe	Gly	Pro	Asn	Gly	Pro	Gln	
240					245					250					255	

BCS 03-5005_PCT-SEQUENZPROTOKOLL.ST25

aca gaa gag gaa cta gaa gca atg cct gat gca gct aca cga tac aaa Thr Glu Glu Glu Leu Glu Ala Met Pro Asp Ala Ala Thr Arg Tyr Lys 260 265 270	817
act tgg aaa gag caa caa aaa gag gat ccg gca agc aat ttg cca tcg Thr Trp Lys Glu Gln Gln Lys Glu Asp Pro Ala Ser Asn Leu Pro Ser 275 280 285	865
tat gat gtg gta gat agt gga aaa gaa tat gat att tac aat att ata Tyr Asp Val Val Asp Ser Gly Lys Glu Tyr Asp Ile Tyr Asn Ile Ile 290 295 300	913
ggt gat cct gaa tcg ttt aag aaa ttt cgt atg aaa cag cct cct att Gly Asp Pro Glu Ser Phe Lys Lys Phe Arg Met Lys Gln Pro Pro Ile 305 310 315	961
gct tac tgg tta gaa act aaa aag gga agg aaa ggc tgg tta cag aaa Ala Tyr Trp Leu Glu Thr Lys Lys Gly Arg Lys Gly Trp Leu Gln Lys 320 325 330 335	1009
tat atg cct gct tta cct cat gga agc aaa tac agg gtg tat ttt aac Tyr Met Pro Ala Leu Pro His Gly Ser Lys Tyr Arg Val Tyr Phe Asn 340 345 350	1057
aca cca aat ggg cct ctt gaa cga gtt cct gcg tgg gcc aat ttt gtc Thr Pro Asn Gly Pro Leu Glu Arg Val Pro Ala Trp Ala Asn Phe Val 355 360 365	1105
att cca gat gca ggc ggg atg gca tta gca gtc cat tgg gaa cca cct Ile Pro Asp Ala Gly Gly Met Ala Leu Ala Val His Trp Glu Pro Pro 370 375 380	1153
cct gaa tat gct tat aaa tgg aaa cac aag cta cca gtc aag cct aag Pro Glu Tyr Ala Tyr Lys Trp Lys His Lys Leu Pro Val Lys Pro Lys 385 390 395	1201
tcc ttg cgc ata tat gaa tgt cat gtt ggc atc tct ggc cag gaa cca Ser Leu Arg Ile Tyr Glu Cys His Val Gly Ile Ser Gly Gln Glu Pro 400 405 410 415	1249
aaa gtt tca tct ttc aat gat ttt att agc aag gtc ctt ccg cat gta Lys Val Ser Ser Phe Asn Asp Phe Ile Ser Lys Val Leu Pro His Val 420 425 430	1297
aaa gaa gct gga tac aat gca ata caa att att gga gtt gtt gag cac Lys Glu Ala Gly Tyr Asn Ala Ile Gln Ile Ile Gly Val Val Glu His 435 440 445	1345
aag gat tat ttc act gtt gga tat aga gtg acc aat ttt tat gct gtt Lys Asp Tyr Phe Thr Val Gly Tyr Arg Val Thr Asn Phe Tyr Ala Val 450 455 460	1393
agt agc cgt tat ggc aca ccg gat gac ttc aag cgc ttg gtt gat gaa Ser Ser Arg Tyr Gly Thr Pro Asp Asp Phe Lys Arg Leu Val Asp Glu 465 470 475	1441
gca cat ggg ctt gga ctg ctt gtc ttt ttg gag att gtg cac tct tat Ala His Gly Leu Gly Leu Leu Val Phe Leu Glu Ile Val His Ser Tyr 480 485 490 495	1489
gca gca gca gat gaa atg gtt ggg tta tct ctt ttt gat gga gca aat Ala Ala Ala Asp Glu Met Val Gly Leu Ser Leu Phe Asp Gly Ala Asn 500 505 510	1537
gat tgc tat ttc cac act ggt aaa cgt gga cac cac aaa ttc tgg ggc Asp Cys Tyr Phe His Thr Gly Lys Arg Gly His His Lys Phe Trp Gly 515 520 525	1585

BCS 03-5005_PCT-SEQUENZPROTOKOLL.ST25

aca	cgg	atg	ttc	aaa	tat	gga	gat	ctt	gat	gtt	ctg	cac	ttt	ctt	ctt	1633
Thr	Arg	Met	Phe	Lys	Tyr	Gly	Asp	Leu	Asp	Val	Leu	His	Phe	Leu	Leu	
		530					535					540				
tca	aat	ctg	aac	tgg	tgg	gtg	gag	gag	tat	cat	gtc	gat	ggc	ttc	cat	1681
Ser	Asn	Leu	Asn	Trp	Trp	Val	Glu	Glu	Tyr	His	Val	Asp	Gly	Phe	His	
	545					550					555					
ttt	cat	tcg	ctc	tcg	tcc	atg	ttg	tat	acg	cat	aat	gga	ttt	gct	tca	1729
Phe	His	Ser	Leu	Ser	Ser	Met	Leu	Tyr	Thr	His	Asn	Gly	Phe	Ala	Ser	
560					565					570					575	
ttt	act	ggt	gac	atg	gat	gaa	tac	tgt	aac	caa	tat	gtt	gac	aag	gag	1777
Phe	Thr	Gly	Asp	Met	Asp	Glu	Tyr	Cys	Asn	Gln	Tyr	Val	Asp	Lys	Glu	
				580					585					590		
gcc	tta	ttg	tac	ctc	ata	tta	gca	aat	gaa	gta	tta	cat	gct	ctt	cat	1825
Ala	Leu	Leu	Tyr	Leu	Ile	Leu	Ala	Asn	Glu	Val	Leu	His	Ala	Leu	His	
			595					600					605			
cct	aat	gtg	atc	acg	att	gct	gag	gat	gca	act	ctg	tat	cct	gga	ctc	1873
Pro	Asn	Val	Ile	Thr	Ile	Ala	Glu	Asp	Ala	Thr	Leu	Tyr	Pro	Gly	Leu	
		610					615					620				
tgc	gat	cca	aca	tct	caa	ggt	gga	ctg	ggc	ttt	gat	tat	ttt	gcc	aat	1921
Cys	Asp	Pro	Thr	Ser	Gln	Gly	Gly	Leu	Gly	Phe	Asp	Tyr	Phe	Ala	Asn	
	625					630					635					
ctt	tct	gcc	tca	gag	atg	tgg	ctt	gca	tta	ctt	gaa	aat	act	cct	gat	1969
Leu	Ser	Ala	Ser	Glu	Met	Trp	Leu	Ala	Leu	Leu	Glu	Asn	Thr	Pro	Asp	
640					645					650					655	
cat	gaa	tgg	tgc	atg	agt	aag	att	gtt	agc	aca	tta	gtg	ggc	gat	aga	2017
His	Glu	Trp	Cys	Met	Ser	Lys	Ile	Val	Ser	Thr	Leu	Val	Gly	Asp	Arg	
				660					665					670		
caa	aat	act	gat	aaa	atg	ctt	ttg	tat	gca	gaa	aat	cac	aac	cag	tcc	2065
Gln	Asn	Thr	Asp	Lys	Met	Leu	Leu	Tyr	Ala	Glu	Asn	His	Asn	Gln	Ser	
			675					680					685			
att	tct	gga	ggt	cgt	tcc	ttc	gca	gaa	ata	ctg	att	ggt	aac	tcc	ttg	2113
Ile	Ser	Gly	Gly	Arg	Ser	Phe	Ala	Glu	Ile	Leu	Ile	Gly	Asn	Ser	Leu	
		690					695					700				
ggg	aaa	tcc	tcc	ata	tca	caa	gag	tca	tta	ctt	aga	ggc	tgc	tcg	tta	2161
Gly	Lys	Ser	Ser	Ile	Ser	Gln	Glu	Ser	Leu	Leu	Arg	Gly	Cys	Ser	Leu	
	705					710					715					
cac	aag	atg	atc	aga	tta	att	aca	tct	aca	att	ggt	ggt	cat	gca	tac	2209
His	Lys	Met	Ile	Arg	Leu	Ile	Thr	Ser	Thr	Ile	Gly	Gly	His	Ala	Tyr	
720					725					730					735	
ctc	aac	ttc	atg	ggc	aat	gaa	ttt	ggt	cac	cca	aag	aga	gta	gag	ttt	2257
Leu	Asn	Phe	Met	Gly	Asn	Glu	Phe	Gly	His	Pro	Lys	Arg	Val	Glu	Phe	
				740					745					750		
cca	atg	tca	agc	aac	aat	ttc	tcc	ttt	tca	ctg	gct	aac	cgt	cgc	tgg	2305
Pro	Met	Ser	Ser	Asn	Asn	Phe	Ser	Phe	Ser	Leu	Ala	Asn	Arg	Arg	Trp	
			755					760					765			
gat	cta	ttg	gaa	gat	gtt	gta	cat	tat	caa	ttg	ttc	tca	ttt	gat	aag	2353
Asp	Leu	Leu	Glu	Asp	Val	Val	His	Tyr	Gln	Leu	Phe	Ser	Phe	Asp	Lys	
		770					775					780				
ggt	atg	atg	gac	ttg	gat	aaa	aat	ggg	aga	att	ttg	tcc	aga	ggt	ctt	2401
Gly	Met	Met	Asp	Leu	Asp	Lys	Asn	Gly	Arg	Ile	Leu	Ser	Arg	Gly	Leu	
	785					790					795					

BCS 03-5005_PCT-SEQUENZPROTOKOLL.ST25

gcc aac att cac cat gtc aat gat act acc atg gtg att tct tac ttg 2449
 Ala Asn Ile His His Val Asn Asp Thr Thr Met Val Ile Ser Tyr Leu
 800 805 810 815
 aga ggt ccc aat ctc ttt gtg ttc aac ttt cat cct gtc aat tca tat 2497
 Arg Gly Pro Asn Leu Phe Val Phe Asn Phe His Pro Val Asn Ser Tyr
 820 825 830
 gaa aga tac att ata ggt gtg gaa gaa gct gga gag tat caa gtc aca 2545
 Glu Arg Tyr Ile Ile Gly Val Glu Glu Ala Gly Glu Tyr Gln Val Thr
 835 840 845
 tta aat aca gat gaa aac aag tat ggt ggt aga gga cta ctt ggc cat 2593
 Leu Asn Thr Asp Glu Asn Lys Tyr Gly Gly Arg Gly Leu Leu Gly His
 850 855 860
 gat cag aat att caa aga acc att agt aga aga gct gat gga atg aga 2641
 Asp Gln Asn Ile Gln Arg Thr Ile Ser Arg Arg Ala Asp Gly Met Arg
 865 870 875
 ttt tgc ttg gaa gtg cct ctg cca agt aga agt gct cag gtc tac aag 2689
 Phe Cys Leu Glu Val Pro Leu Pro Ser Arg Ser Ala Gln Val Tyr Lys
 880 885 890 895
 ttg acc cga att cta aga gca tgatcactct agtaatcaaa gtgcctcata 2740
 Leu Thr Arg Ile Leu Arg Ala
 900
 tgatgacaca aaaggaaagg ttctacattg cccttacact gatcaatatt gacacctttc 2800
 cgagggtgagt ttctgtgatt cttgagcaga ctgttggtgta gtcaattatc atgaactttt 2860
 gccttcagca tccggatagt cgcttctcct gtgcaatgag ggcatggacg aatttttttt 2920
 tggcttgta tgggggtcat aagcatccgc cagattaaga ttccacaggc ctcgagtaaa 2980
 accatcactt actttaagga tacacaaaca caccaacggg gtgcaggctc tgataccttc 3040
 taaagtg 3047

<210> 6

<211> 902

<212> PRT

<213> solanum tuberosum

<400> 6

Met Leu Ser Leu Ser Asp Ser Ile Arg Ile Ser Ser Pro Leu Ser Asp
 1 5 10 15

Ser Arg Leu Ser Phe Leu Ser Gln Thr Gly Ser Arg Thr Ser Arg Gln
 20 25 30

Leu Lys Phe Val Arg Ser Arg Arg Ala Arg Val Ser Arg Cys Arg Cys
 35 40 45

Ser Ala Thr Glu Gln Pro Pro Pro Gln Arg Arg Lys Gln Arg Pro Glu
 50 55 60

BCS 03-5005_PCT-SEQUENZPROTOKOLL.ST25

Lys Tyr Lys Gln Ser Glu Glu Gly Lys Gly Ile Asp Pro Val Gly Phe
65 70 75 80

Leu Ser Lys Tyr Gly Ile Thr His Lys Ala Phe Ala Gln Phe Leu Arg
85 90 95

Glu Arg Tyr Lys Ser Leu Lys Asp Leu Lys Asp Glu Ile Leu Thr Arg
100 105 110

His Phe Ser Leu Lys Glu Met Ser Thr Gly Tyr Glu Leu Met Gly Met
115 120 125

His Arg Asn Ile Gln His Arg Val Asp Phe Leu Glu Trp Ala Pro Gly
130 135 140

Ala Arg Tyr Cys Ala Leu Ile Gly Asp Phe Asn Gly Trp Ser Thr Thr
145 150 155 160

Gly Asn Cys Ala Arg Glu Gly His Phe Gly His Asp Asp Tyr Gly Tyr
165 170 175

Trp Phe Ile Ile Leu Glu Asp Lys Leu Arg Glu Gly Glu Glu Pro Asp
180 185 190

Lys Leu Tyr Phe Gln Gln Tyr Asn Tyr Ala Glu Asp Tyr Gly Lys Gly
195 200 205

Asp Thr Gly Ile Thr Val Glu Glu Ile Phe Lys Lys Ala Asn Asp Glu
210 215 220

Tyr Trp Glu Pro Gly Glu Asp Arg Phe Ile Lys Ser Arg Tyr Glu Val
225 230 235 240

Ala Ala Lys Leu Tyr Glu Glu Met Phe Gly Pro Asn Gly Pro Gln Thr
245 250 255

Glu Glu Glu Leu Glu Ala Met Pro Asp Ala Ala Thr Arg Tyr Lys Thr
260 265 270

Trp Lys Glu Gln Gln Lys Glu Asp Pro Ala Ser Asn Leu Pro Ser Tyr
275 280 285

Asp Val Val Asp Ser Gly Lys Glu Tyr Asp Ile Tyr Asn Ile Ile Gly
290 295 300

Asp Pro Glu Ser Phe Lys Lys Phe Arg Met Lys Gln Pro Pro Ile Ala
305 310 315 320

Tyr Trp Leu Glu Thr Lys Lys Gly Arg Lys Gly Trp Leu Gln Lys Tyr
325 330 335

BCS 03-5005_PCT-SEQUENZPROTOKOLL.ST25

Met Pro Ala Leu Pro His Gly Ser Lys Tyr Arg Val Tyr Phe Asn Thr
 340 345 350

Pro Asn Gly Pro Leu Glu Arg Val Pro Ala Trp Ala Asn Phe Val Ile
 355 360 365

Pro Asp Ala Gly Gly Met Ala Leu Ala Val His Trp Glu Pro Pro Pro
 370 375 380

Glu Tyr Ala Tyr Lys Trp Lys His Lys Leu Pro Val Lys Pro Lys Ser
 385 390 395 400

Leu Arg Ile Tyr Glu Cys His Val Gly Ile Ser Gly Gln Glu Pro Lys
 405 410 415

Val Ser Ser Phe Asn Asp Phe Ile Ser Lys Val Leu Pro His Val Lys
 420 425 430

Glu Ala Gly Tyr Asn Ala Ile Gln Ile Ile Gly Val Val Glu His Lys
 435 440 445

Asp Tyr Phe Thr Val Gly Tyr Arg Val Thr Asn Phe Tyr Ala Val Ser
 450 455 460

Ser Arg Tyr Gly Thr Pro Asp Asp Phe Lys Arg Leu Val Asp Glu Ala
 465 470 475 480

His Gly Leu Gly Leu Leu Val Phe Leu Glu Ile Val His Ser Tyr Ala
 485 490 495

Ala Ala Asp Glu Met Val Gly Leu Ser Leu Phe Asp Gly Ala Asn Asp
 500 505 510

Cys Tyr Phe His Thr Gly Lys Arg Gly His His Lys Phe Trp Gly Thr
 515 520 525

Arg Met Phe Lys Tyr Gly Asp Leu Asp Val Leu His Phe Leu Leu Ser
 530 535 540

Asn Leu Asn Trp Trp Val Glu Glu Tyr His Val Asp Gly Phe His Phe
 545 550 555 560

His Ser Leu Ser Ser Met Leu Tyr Thr His Asn Gly Phe Ala Ser Phe
 565 570 575

Thr Gly Asp Met Asp Glu Tyr Cys Asn Gln Tyr Val Asp Lys Glu Ala
 580 585 590

Leu Leu Tyr Leu Ile Leu Ala Asn Glu Val Leu His Ala Leu His Pro
 595 600 605



PCT/EP2004/010984

BCS 03-5005_PCT-SEQUENZPROTOKOLL.ST25

Gln Asn Ile Gln Arg Thr Ile Ser Arg Arg Ala Asp Gly Met Arg Phe
865 870 875 880

BCS 03-5005_PCT-SEQUENZPROTOKOLL.ST25

Cys Leu Glu Val Pro Leu Pro Ser Arg Ser Ala Gln Val Tyr Lys Leu
885 890 895

Thr Arg Ile Leu Arg Ala
900